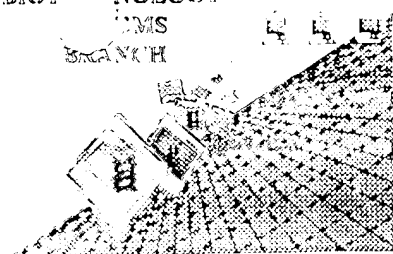


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/719,379
Source: Pct 09
Date Processed by STIC: 2-15-2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/719,379

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☒ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.
- 12 ☒ Use of <220>Feature (NEW RULES) Sequence(s) 73 are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.
AKS-Biotechnology Systems Branch- 5/15/99

PCT09

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/719,379

DATE: 02/15/2001
 TIME: 14:29:54

Input Set : A:\seqlist.txt
 Output Set: N:\CRF3\02152001\I719379.raw

**Does Not Comply
 Corrected Diskette Needed**

4 <110> APPLICANT: Joe Cohen
 5 Yves Lobet
 6 Guy Dequesne
 7 Lauren Bakaletz
 9 <120> TITLE OF INVENTION: Vaccine
 12 <130> FILE REFERENCE: B45145
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/719,379
 C--> 14 <141> CURRENT FILING DATE: 2000-12-11
 14 <160> NUMBER OF SEQ ID NOS: 81
 16 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 19
 20 <212> TYPE: PRT
 21 <213> ORGANISM: Haemophilus influenzae strain ntHi-10567RM
 23 <400> SEQUENCE: 1
 24 Arg Ser Asp Tyr Lys Phe Tyr Glu Ala Ala Asn Gly Thr Arg Asp His
 25 1 5 10 15
 26 Lys Lys Gly
 29 <210> SEQ ID NO: 2
 30 <211> LENGTH: 22
 31 <212> TYPE: PRT
 32 <213> ORGANISM: Haemophilus influenzae strain ntHi-1715MEE
 34 <400> SEQUENCE: 2
 35 Arg Ser Asp Tyr Lys Leu Tyr Asn Lys Asn Ser Ser Ser Asn Ser Thr
 36 1 5 10 15
 37 Leu Lys Asn Leu Gly Glu
 38 20
 40 <210> SEQ ID NO: 3
 41 <211> LENGTH: 13
 42 <212> TYPE: PRT
 43 <213> ORGANISM: Haemophilus influenzae strain ntHi-1729MEE
 45 <400> SEQUENCE: 3
 46 Arg Ser Asp Tyr Lys Phe Tyr Asp Asn Lys Arg Ile Asp
 47 1 5 10
 49 <210> SEQ ID NO: 4
 50 <211> LENGTH: 19
 51 <212> TYPE: PRT
 52 <213> ORGANISM: Haemophilus influenzae strain ntHi-183NP
 54 <400> SEQUENCE: 4
 55 Arg Ser Asp Tyr Lys Leu Tyr Asn Lys Asn Ser Ser Thr Leu Lys Asp
 56 1 5 10 15
 57 Leu Gly Glu
 60 <210> SEQ ID NO: 5
 61 <211> LENGTH: 19
 62 <212> TYPE: PRT
 63 <213> ORGANISM: Haemophilus influenzae strain ntHi-1128
 65 <400> SEQUENCE: 5

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/719,379

DATE: 02/15/2001
TIME: 14:29:54

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\02152001\I719379.raw

66 Arg Ser Asp Tyr Lys Phe Tyr Glu Asp Ala Asn Gly Thr Arg Asp His
67 1 5 10 15
68 Lys Lys Gly
71 <210> SEQ ID NO: 6
72 <211> LENGTH: 19
73 <212> TYPE: PRT
74 <213> ORGANISM: Non-typable Haemophilus influenzae
76 <400> SEQUENCE: 6
W--> 77 Arg Ser Asp Tyr Lys Phe Tyr Glu Ala Pro Asn Ser Thr Arg Asp Xaa
78 1 5 10 15
79 Lys Lys Gly
82 <210> SEQ ID NO: 7
83 <211> LENGTH: 19
84 <212> TYPE: PRT
85 <213> ORGANISM: Haemophilus influenzae strain ntHi-152NP
87 <400> SEQUENCE: 7
88 Arg Ser Asp Tyr Lys Phe Tyr Glu Asp Ala Asp Gly Thr Arg Asp His
89 1 5 10 15
90 Lys Lys Gly
93 <210> SEQ ID NO: 8
94 <211> LENGTH: 19
95 <212> TYPE: PRT
96 <213> ORGANISM: Haemophilus influenzae strain ntHi-1234MEE
98 <400> SEQUENCE: 8
99 Arg Ser Asp Tyr Lys Phe Tyr Asp Asp Ala Asn Gly Thr Arg Asp His
100 1 5 10 15
101 Lys Lys Gly
104 <210> SEQ ID NO: 9
105 <211> LENGTH: 19
106 <212> TYPE: PRT
107 <213> ORGANISM: Haemophilus influenzae strain ntHi-90100RM
109 <400> SEQUENCE: 9
110 Arg Ser Asp Tyr Lys Phe Tyr Glu Asp Glu Asn Gly Thr Arg Asp His
111 1 5 10 15
112 Lys Lys Gly
115 <210> SEQ ID NO: 10
116 <211> LENGTH: 19
117 <212> TYPE: PRT
118 <213> ORGANISM: Haemophilus influenzae strain ntHi-86027NP
120 <400> SEQUENCE: 10
121 Arg Ser Asp Tyr Lys Phe Tyr Glu Val Ala Asn Gly Thr Arg Asp His
122 1 5 10 15
123 Lys Lys Gly
126 <210> SEQ ID NO: 11
127 <211> LENGTH: 19
128 <212> TYPE: PRT
129 <213> ORGANISM: Haemophilus influenzae strain ntHi-476
131 <400> SEQUENCE: 11
132 Arg Ser Asp Tyr Lys Phe Tyr Glu Glu Ala Asn Gly Thr Arg Asp His

Use of "Xaa"
requires mandatory
numeric identifiers
<220>, <221>, <222>, and
<223>.
See item 10. a
ERROR SUMMARY
SHEET

RAW SEQUENCE LISTING DATE: 02/15/2001
 PATENT APPLICATION: US/09/719,379 TIME: 14:29:54

Input Set : A:\seqlist.txt
 Output Set: N:\CRF3\02152001\I719379.raw

```

133   1               5               10               15
134   Lys Lys Gly
137 <210> SEQ ID NO: 12
138 <211> LENGTH: 19
139 <212> TYPE: PRT
140 <213> ORGANISM: Haemophilus influenzae strain ntHi-166NP
142 <400> SEQUENCE: 12
143   Arg Ser Asp Tyr Lys Phe Tyr Asn Asp Ala Asn Gly Thr Arg Asp His
144   1               5               10               15
145   Lys Lys Ser
148 <210> SEQ ID NO: 13
149 <211> LENGTH: 19
150 <212> TYPE: PRT
151 <213> ORGANISM: Haemophilus influenzae strain ntHi-1848NP
153 <400> SEQUENCE: 13
154   Arg Ser Asp Tyr Lys Phe Tyr Glu Val Ala Asn Gly Thr Arg Asp His
155   1               5               10               15
156   Lys Lys Ser
159 <210> SEQ ID NO: 14
160 <211> LENGTH: 19
161 <212> TYPE: PRT
162 <213> ORGANISM: Haemophilus influenzae strain ntHi-567
164 <400> SEQUENCE: 14
165   Arg Ser Asp Tyr Lys Phe Tyr Glu Asp Ala Asn Gly Thr Arg Asp Arg
166   1               5               10               15
167   Lys Thr Gly
170 <210> SEQ ID NO: 15
171 <211> LENGTH: 19
172 <212> TYPE: PRT
173 <213> ORGANISM: Haemophilus influenzae strain ntHi-484
175 <400> SEQUENCE: 15
176   Arg Ser Asp Tyr Lys Phe Tyr Glu Asp Ala Asn Gly Thr Arg Lys His
177   1               5               10               15
178   Lys Glu Gly
181 <210> SEQ ID NO: 16
182 <211> LENGTH: 19
183 <212> TYPE: PRT
184 <213> ORGANISM: Haemophilus influenzae strain ntHi-10559RM
186 <400> SEQUENCE: 16
187   Arg Ser Asp Tyr Lys Leu Tyr Glu Val Ala Asn Gly Thr Arg Asp His
188   1               5               10               15
189   Lys Lys Ser
192 <210> SEQ ID NO: 17
193 <211> LENGTH: 19
194 <212> TYPE: PRT
195 <213> ORGANISM: Haemophilus influenzae strain ntHi-601
197 <400> SEQUENCE: 17
198   Arg Ser Asp Tyr Lys Phe Tyr Glu Val Ala Asn Gly Thr Arg Asp His
199   1               5               10               15

```

RAW SEQUENCE LISTING DATE: 02/15/2001
 PATENT APPLICATION: US/09/719,379 TIME: 14:29:54

Input Set : A:\seqlist.txt
 Output Set: N:\CRF3\02152001\I719379.raw

```

200 Lys Gln Ser
203 <210> SEQ ID NO: 18
204 <211> LENGTH: 19
205 <212> TYPE: PRT
206 <213> ORGANISM: Haemophilus influenzae strain ntHi-226NP
208 <400> SEQUENCE: 18
209 Arg Ser Asp Tyr Lys Phe Tyr Glu Glu Ala Asn Gly Thr Arg Asp His
210 1 5 10 15
211 Lys Arg Ser
214 <210> SEQ ID NO: 19
215 <211> LENGTH: 19
216 <212> TYPE: PRT
217 <213> ORGANISM: Haemophilus influenzae strain ntHi-480
219 <400> SEQUENCE: 19
220 Arg Ser Asp Tyr Lys Phe Tyr Glu Asp Ala Asn Gly Thr Arg Glu Arg
221 1 5 10 15
222 Lys Arg Gly
225 <210> SEQ ID NO: 20
226 <211> LENGTH: 19
227 <212> TYPE: PRT
228 <213> ORGANISM: Haemophilus influenzae strain ntHi-1657MEE
230 <400> SEQUENCE: 20
231 Arg Ser Asp Tyr Lys Phe Tyr Glu Val Ala Asn Gly Thr Arg Glu Arg
232 1 5 10 15
233 Lys Lys Gly
236 <210> SEQ ID NO: 21
237 <211> LENGTH: 19
238 <212> TYPE: PRT
239 <213> ORGANISM: Haemophilus influenzae strain ntHi-214NP
241 <400> SEQUENCE: 21
242 Arg Ser Asp Tyr Lys Phe Tyr Glu Val Pro Asn Gly Thr Arg Asp His
243 1 5 10 15
244 Lys Gln Ser
247 <210> SEQ ID NO: 22
248 <211> LENGTH: 19
249 <212> TYPE: PRT
250 <213> ORGANISM: Haemophilus influenzae strain ntHi-250NP
252 <400> SEQUENCE: 22
253 Arg Ser Asp Tyr Lys Arg Tyr Glu Glu Ala Asn Gly Thr Arg Asn His
254 1 5 10 15
255 Asp Lys Gly
258 <210> SEQ ID NO: 23
259 <211> LENGTH: 19
260 <212> TYPE: PRT
261 <213> ORGANISM: Haemophilus influenzae strain ntHi-499
263 <400> SEQUENCE: 23
264 Arg Ser Asp Tyr Glu Phe Tyr Glu Ala Pro Asn Ser Thr Arg Asp His
265 1 5 10 15
266 Lys Lys Gly

```

RAW SEQUENCE LISTING DATE: 02/15/2001
 PATENT APPLICATION: US/09/719,379 TIME: 14:29:54

Input Set : A:\seqlist.txt
 Output Set: N:\CRF3\02152001\I719379.raw

```

269 <210> SEQ ID NO: 24
270 <211> LENGTH: 21
271 <212> TYPE: PRT
272 <213> ORGANISM: Haemophilus influenzae strain ntHi-492
274 <400> SEQUENCE: 24
275 Arg Ser Asp Tyr Lys Leu Tyr Asn Lys Asn Ser Ser Asn Ser Thr Leu
276 1 5 10 15
277 Lys Asn Leu Gly Glu
278 20
280 <210> SEQ ID NO: 25
281 <211> LENGTH: 21
282 <212> TYPE: PRT
283 <213> ORGANISM: Haemophilus influenzae strain ntHi-502
285 <400> SEQUENCE: 25
286 Arg Ser Asp Tyr Lys Leu Tyr Asp Lys Asn Ser Ser Ser Asn Thr Leu
287 1 5 10 15
288 Lys Lys Leu Gly Glu
289 20
291 <210> SEQ ID NO: 26
292 <211> LENGTH: 20
293 <212> TYPE: PRT
294 <213> ORGANISM: Haemophilus influenzae strain ntHi-165NP
296 <400> SEQUENCE: 26
297 Arg Ser Asp Tyr Lys Leu Tyr Asn Lys Asn Ser Ser Asn Thr Leu Lys
298 1 5 10 15
299 Asp Leu Gly Glu
300 20
302 <210> SEQ ID NO: 27
303 <211> LENGTH: 20
304 <212> TYPE: PRT
305 <213> ORGANISM: Haemophilus influenzae strain ntHi-495
307 <400> SEQUENCE: 27
308 Arg Ser Asp Tyr Lys Leu Tyr Asn Lys Asn Ser Ser Asp Ala Leu Lys
309 1 5 10 15
310 Lys Leu Gly Glu
311 20
313 <210> SEQ ID NO: 28
314 <211> LENGTH: 40
315 <212> TYPE: PRT
316 <213> ORGANISM: LB1 peptide (derived from Haemophilus influenzae)
318 <400> SEQUENCE: 28
319 Arg Ser Asp Tyr Lys Phe Tyr Glu Asp Ala Asn Gly Thr Arg Asp His
320 1 5 10 15
321 Lys Lys Gly Pro Ser Leu Lys Leu Leu Ser Leu Ile Lys Gly Val Ile
322 20 25 30
323 Val His Arg Leu Glu Gly Val Glu
324 35 40
326 <210> SEQ ID NO: 29
327 <211> LENGTH: 57

```

<213> Artificial Sequence - see Figure 1

numeric identifier <213> must only be "Artificial Sequence" and requires use of numeric identifiers <220>, and <223>

<400> 73

```
ctcttacaca ttccagccct gaaaaagggc atcaaattaa accacacctt aaggaggata 60
taacatatgg atcccatggc cacgtgtgat cagagctcaa ctagtggccca ccatcaccat 120
caccattaat ctagaatcga taagcttcga ccgatgcc 158
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<210> 74

<211> 1244

<212> DNA

<213> Haemophilus influenzae - see Figure 2

<220>

<221> CDS

<222> (67)...(1212)

<400> 74

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ctcttacaca ttccagccct gaaaaagggc atcaaattaa accacacctt aaggaggata 60
taacat atg gat cca aaa act tta gcc ctt tct tta tta gca gct ggc 108
Met Asp Pro Lys Thr Leu Ala Leu Ser Leu Leu Ala Ala Gly
1 5 10
```

```
gta cta gca ggt tgt agc agc cat tca tca aat atg gcg aat acc caa 156
Val Leu Ala Gly Cys Ser Ser His Ser Ser Asn Met Ala Asn Thr Gln
15 20 25 30
```

```
atg aaa tca gac aaa atc att att gct cac cgt ggt gct agc ggt tat 204
Met Lys Ser Asp Lys Ile Ile Ile Ala His Arg Gly Ala Ser Gly Tyr
35 40 45
```

```
tta cca gag cat acg tta gaa tct aaa gca ctt gcg ttt gca caa cag 252
Leu Pro Glu His Thr Leu Glu Ser Lys Ala Leu Ala Phe Ala Gln Gln
50 55 60
```

```
gct gat tat tta gag caa gat tta gca atg act aag gat ggt cgt tta 300
Ala Asp Tyr Leu Glu Gln Asp Leu Ala Met Thr Lys Asp Gly Arg Leu
65 70 75
```

```
gtg gtt att cac gat cac ttt tta gat ggc ttg act gat gtt gcg aaa 348
Val Val Ile His Asp His Phe Leu Asp Gly Leu Thr Asp Val Ala Lys
80 85 90
```

```
aaa ttc cca cat cgt cat cgt aaa gat ggc cgt tac tat gtc atc gac 396
Lys Phe Pro His Arg His Arg Lys Asp Gly Arg Tyr Tyr Val Ile Asp
95 100 105 110
```

```
ttt acc tta aaa gaa att caa agt tta gaa atg aca gaa aac ttt gaa 444
Phe Thr Leu Lys Glu Ile Gln Ser Leu Glu Met Thr Glu Asn Phe Glu
115 120 125
```

```
acc aaa gat ggc aaa caa gcg caa gtt tat cct aat cgt ttc cct ctt 492
Thr Lys Asp Gly Lys Gln Ala Gln Val Tyr Pro Asn Arg Phe Pro Leu
130 135 140
```

```
tgg aaa tca cat ttt aga att cat acc ttt gaa gat gaa att gaa ttt 540
Trp Lys Ser His Phe Arg Ile His Thr Phe Glu Asp Glu Ile Glu Phe
145 150 155
```

see item 12 on
EXROR Summary
sheet.

VERIFICATION SUMMARY

DATE: 02/15/2001

PATENT APPLICATION: US/09/719,379

TIME: 14:29:55

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\02152001\I719379.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:77 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:77 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:77 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:77 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:77 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:687 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:687 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: